Exhibit C
Blast of SEQ ID NO: 1 versus human genome

MEGABLAST 1.2.3-Paracel [2001-11-20]

Reference:
Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000),
"A greedy algorithm for aligning DNA sequences",
J Comput Biol 2000; 7(1-2):203-14.
Database: Homo_sapiens.latestgp.masked.fa
          33,840 sequences; 200,810,911,373 total letters

Query= LEX121seqid1
        (747 letters)

	Score (bits)	E Value
Sequences producing significant alignments:		
AC135034.1.27032.29361	287	5e-75
AC025418.23.1.83000	287	5e-75
AC135034.1.59399.65233	174	5e-41

>AC135034.1.27032.29361
          Length = 2330

 Score = 287 bits (145), Expect = 5e-75
 Identities = 145/145 (100%)
 Strand = Plus / Plus

```
Query: 451   ttacagtgttgtggccaacataattacacagactggataaagaataagaacaaagaaaat 510
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1180  ttacagtgttgtggccaacataattacacagactggataaagaataagaacaaagaaaat 1239


Query: 511   tcaggacaggtgccatgttcttgcacaaagtcaactttaagaaaatggttttgtgatgag 570
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1240  tcaggacaggtgccatgttcttgcacaaagtcaactttaagaaaatggttttgtgatgag 1299


Query: 571   ccactgaatgcaacttaccttgagg 595
             |||||||||||||||||||||||||
Sbjct: 1300  ccactgaatgcaacttaccttgagg 1324
```

>AC025418.23.1.83000
          Length = 83000

 Score = 287 bits (145), Expect = 5e-75
 Identities = 145/145 (100%)
 Strand = Plus / Minus

```
Query: 451   ttacagtgttgtggccaacataattacacagactggataaagaataagaacaaagaaaat 510
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 48068 ttacagtgttgtggccaacataattacacagactggataaagaataagaacaaagaaaat 48009
```

```
Query: 511   tcaggacaggtgccatgttcttgcacaaagtcaacttaagaaatggttttgtgatgag 570
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 48008 tcaggacaggtgccatgttcttgcacaaagtcaactttaagaaaatggttttgtgatgag 47949


Query: 571   ccactgaatgcaacttaccttgagg 595
             |||||||||||||||||||||||||
Sbjct: 47948 ccactgaatgcaacttaccttgagg 47924



 Score =  250 bits (126), Expect = 1e-63
 Identities = 126/126 (100%)
 Strand = Plus / Minus


Query: 139   gatgaaaataatcacttcatagtacctatttctcaaattttgattggaatgggatcttct 198
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 58492 gatgaaaataatcacttcatagtacctatttctcaaattttgattggaatgggatcttct 58433


Query: 199   actgttctttttgtctattgggttatataggaattcacaacgaaatcagatggctccta 258
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 58432 actgttctttttgtctattgggttatataggaattcacaacgaaatcagatggctccta 58373


Query: 259   attgtg 264
             ||||||
Sbjct: 58372 attgtg 58367



 Score =  224 bits (113), Expect = 6e-56
 Identities = 113/113 (100%)
 Strand = Plus / Minus


Query: 338   aggttcagcaactatggcatgacaaaattgattttgtcatttctgagtatggatctaaag 397
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 50207 aggttcagcaactatggcatgacaaaattgattttgtcatttctgagtatggatctaaag 50148


Query: 398   ataagcctgaagatataaccaagtggactattctgaatgccttacagaaaaca 450
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 50147 ataagcctgaagatataaccaagtggactattctgaatgccttacagaaaaca 50095



 Score =  174 bits (88), Expect = 5e-41
 Identities = 88/88 (100%)
 Strand = Plus / Minus


Query: 593   agggttgtgaaaataaaatcagtgcatggtataatgttaatgtgttaaccttaatcggaa 652
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 46442 agggttgtgaaaataaaatcagtgcatggtataatgttaatgtgttaaccttaatcggaa 46383


Query: 653   ttaactttggactttaacttcagaggt 680
             |||||||||||||||||||||||||||
```

Sbjct: 46382 ttaactttg●tttttaacttcagaggt 46355   ●

Score = 155 bits (78), Expect = 5e-35
Identities = 78/78 (100%)
Strand = Plus / Minus

Query: 264   gtatgcagtattgataacatggacctttgctgttcaggttgtactttcagcattcatcat 323
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 53869 gtatgcagtattgataacatggacctttgctgttcaggttgtactttcagcattcatcat 53810

Query: 324   cacaaagaaagaggaggt 341
             ||||||||||||||||||
Sbjct: 53809 cacaaagaaagaggaggt 53792

Score = 147 bits (74), Expect = 1e-32
Identities = 74/74 (100%)
Strand = Plus / Minus

Query: 66   ggttcttggacttttattcatgggatttggtgcatggctcttattagatagaaataattt 125
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 60260 ggttcttggacttttattcatgggatttggtgcatggctcttattagatagaaataattt 60201

Query: 126   tttaacagcttttg 139
             ||||||||||||||
Sbjct: 60200 tttaacagcttttg 60187

Score = 141 bits (71), Expect = 7e-31
Identities = 71/71 (100%)
Strand = Plus / Minus

Query: 677   aggttttccaagtctcattaacagtttgtttcttcaaaaacatcaagaatataatccatg 736
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 45026 aggttttccaagtctcattaacagtttgtttcttcaaaaacatcaagaatataatccatg 44967

Query: 737   cagaaatgtga 747
             |||||||||||
Sbjct: 44966 cagaaatgtga 44956

Score = 135 bits (68), Expect = 4e-29
Identities = 68/68 (100%)
Strand = Plus / Minus

Query: 1   atgttaagaaataacaaaacaataattattaagtactttcttaatctcattaatggagct 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 60414 atgttaagaaataacaaaacaataattattaagtactttcttaatctcattaatggagct 60355

```
Query: 61     ttcttggt
              ||·|||||
Sbjct: 60354 ttcttggt 60347


>AC135034.1.59399.65233
          Length = 5835

 Score =  174 bits (88), Expect = 5e-41
 Identities = 88/88 (100%)
 Strand = Plus / Minus


Query: 593   agggttgtgaaaataaaatcagtgcatggtataatgttaatgtgttaaccttaatcggaa 652
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 5352  agggttgtgaaaataaaatcagtgcatggtataatgttaatgtgttaaccttaatcggaa 5293


Query: 653   ttaactttggactttttaacttcagaggt 680
             |||||||||||||||||||||||||||||
Sbjct: 5292  ttaactttggactttttaacttcagaggt 5265



 Score =  141 bits (71), Expect = 7e-31
 Identities = 71/71 (100%)
 Strand = Plus / Minus


Query: 677   aggttttccaagtctcattaacagtttgtttcttcaaaaacatcaagaatataatccatg 736
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3942  aggttttccaagtctcattaacagtttgtttcttcaaaaacatcaagaatataatccatg 3883


Query: 737   cagaaatgtga 747
             |||||||||||
Sbjct: 3882  cagaaatgtga 3872
```